



# Blast 2 Sequences results

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Structure

## BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.13 [Nov-27-2005]

Matrix BLOSUM62 gap open: 11 gap extension: 1

x\_dropoff: 50 expect: 10.0000 wordsize: 3 Filter ☐ View option Standard

Masking character option X for protein, n for nucleotide Masking color option Black

☐ Show CDS translation 

Sequence 1: lcl|Navarro

Length = 569 (1 .. 569)

Sequence 2: lcl|Watson

Length = 566 (1 .. 566)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

Score = 883 bits (2281), Expect = 0.0  
 Identities = 454/559 (81%), Positives = 475/559 (84%), Gaps = 21/559 (3%)

```

Query   24   PTCVLSQVQLKESGPGLVKPSQTLSTCTVSGLSLSSNSVGWVRQAPGKGLEWVGRSGG   83
          PTC  SQVQLKESGPGLVKPSQTLSTCTVSG SL+S +VGWV +  K  +
Sbjct   16   PTCAPSQVQLKESGPGLVKPSQTLSTCTVSGFSLTSYTVGWVARLQEKDWNMLRLYVIV   75

Query   84   EEEYYNPALKSRATITEDAAKSQVYLDAEQVTGEATAVYYCAEV-----YNNYLYYGI   136
          +   LKSRA+IT DA+KSQVYL  +T E TAVYYCA          Y+  Y+G
Sbjct   76   GVQTSTQTLKSRASITRDASKSQVYLTLSLTVEDTAVYYCARSLPVSGNGYSLVNYWGQ   135

Query   137  KELGARGLLVTVSSSVSKQAPLIFPLAACCKDTKTTNITLGCLVKGYFPG----AWDAGPL   192
          VTVSSSVSKQ+P+I PLAACCKDTKTTNITLGCLVKGYFP          WDAG L
Sbjct   136  AS-----VTVSSSVSKQSPIILPLAACCKDTKTTNITLGCLVKGYFPEPVTVTWDAGSL   188

Query   193  NPSTMTFPAVFDQTSGLYTTISRNVASGKWAKQKFTCGVVHSQETFNKTFFNACIVTFTPP   252
          N ST+TFPAVFDQTSGLYTTISRNVASGKWAKQKFTC VVHSQETFNKTFFNACIVTFTPP
Sbjct   189  NRSTITFPAVFDQTSGLYTTISRNVASGKWAKQKFTCNVHSQETFNKTFFNACIVTFTPP   248
  
```

## EXHIBIT A

```

Query 253 TVKLFHSSCDPGGDSHTTIQLLCLISDYTPGDIDIVWLIIEGQKVDEQFPTQASMKQEGSW 312
          TVKLFHSSCDPGGDSHTTIQLLCLISDYTPGDIDIVWLI+GQKVDEQFP      +KQEG
Sbjct 249 TVKLFHSSCDPGGDSHTTIQLLCLISDYTPGDIDIVWLIDGQKVDEQFPQHGLVKQEGKL 308

Query 313 PPTHSELNINQGQWASENTYTCQVTYK--DMIFNQARKCTESDPPGVSVYLSPPSPDL DY 370
          THSELNI QGQWASENTYTCQVTYK D++ + RKCTES+P GVSVYLSPPSPDL DY
Sbjct 309 ASTHSELNITQGQWASENTYTCQVTYKRHDLRLTRPRKCTESEPRGVSVYLSPPSPDL DY 368

Query 371 VSKTPKITCLVVDLANVQGLSLNWSRESGEPLQKHTLATSEQFNKTFSVTSTLPVDTTDW 430
          VSK+PKITCLVVDLANVQGLSLNWSRESGEPLQKHTLATSEQFNKTFSVTSTLPVDTTDW
Sbjct 369 VSKSPKITCLVVDLANVQGLSLNWSRESGEPLQKHTLATSEQFNKTFSVTSTLPVDTTDW 428

Query 431 IEGETYKCTVSHPDLPREVVRSAKAPGKRLSPEVYVFLPPEEDQSSKDKVTLTCLIQNF 490
          IEGETYKCTVSHPDLPREVVRSAKAPGKRLSPEVYVFLPPEEDQSSKDKVTLTCLIQNF
Sbjct 429 IEGETYKCTVSHPDLPREVVRSAKAPGKRLSPEVYVFLPPEEDQSSKDKVTLTCLIQNF 488

Query 491 FPADISVQWRRNNVLIQTDQQATTRPQKANGPDPAFFVFSRLEVSRAEWEQKNKFACKVV 550
          FPADISVQW RNNVLIQTDQQATTRP K+ P PAFFVFSRLEVSRAEWEQKNKFACKVV
Sbjct 489 FPADISVQWLRNNVLIQTDQQATTRP-KSQWPRPAFFVFSRLEVSRAEWEQKNKFACKVV 547

Query 551 HEALSQRTLQKEVSKDPGK 569
          HEALSQRTLQKEVSKDPGK
Sbjct 548 HEALSQRTLQKEVSKDPGK 566

```

CPU time: 0.04 user secs. 0.01 sys. secs 0.05 total secs.

Lambda K H  
0.315 0.131 0.398

Gapped  
Lambda K H  
0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 1

Number of Hits to DB: 2833

Number of extensions: 1496

Number of successful extensions: 20

Number of sequences better than 10.0: 1

Number of HSP's gapped: 1

Number of HSP's successfully gapped: 1

Length of query: 569

Length of database: 1,125,694,017

Length adjustment: 138

Effective length of query: 431

Effective length of database: 1,125,693,879

Effective search space: 485174061849

Effective search space used: 485174061849

Neighboring words threshold: 9

X1: 16 ( 7.3 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 41 (21.6 bits)

S2: 81 (35.8 bits)

